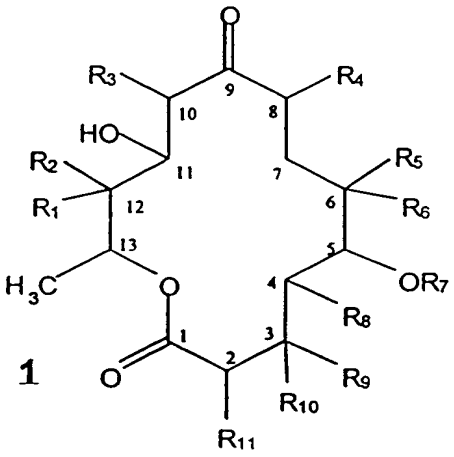
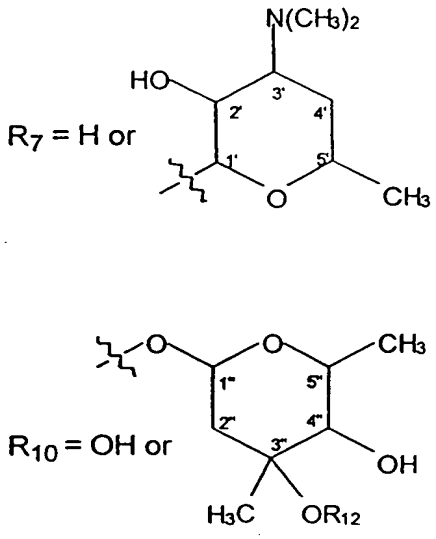




A1 CONT.

or a pharmaceutically acceptable salt thereof, wherein R_1 is H or OH; R_2-R_4 are each independently H, CH_3, or CH_2CH_3; R_5 is H or OH; and R_6 is H, CH_3, or CH_2CH_3; R_7 is H or desosamine; R_8 is H, CH_3, or CH_2CH_3; R_9 is OH, mycarose (R_{12} is H), or cladinose (R_{12} is CH_3), R_{10} is H; or R_9 = R_{10} = O; and R_{11} is H, CH_3, or CH_2CH_3, with the proviso that when R_2-R_4 are CH_3, R_6 is CH_3, R_8 is CH_3, and R_{11} is CH_3, then R_1 and R_5 are not H and R_{12} is not H; or also when R_2-R_4 are CH_3, R_6 is CH_3, R_8 is CH_3, and R_{11} is CH_3, then R_1 and R_5 are not OH and R_{12} is not H.

Claim 12, line 1, delete "or 11".

Claim 13, line 1, delete ", 11 or 12".

Claim 14, line 1, delete ", 11 or 12".

Claim 16, line 1, delete "any of claims 10-15" and insert therefor --claim 10--.

Claim 17, line 1, delete "any of claims 10-16" and insert therefor --claim 10--.

Claim 18, line 1, delete "any of claims 10-13, 16 or 17" and insert therefor --claim 10--.

Claim 20, line 2, delete "19" and insert therefor --26--.

Claim 22, line 2, delete "any of claims 10-18" and insert therefor --claim 10--.

A2

25. (Amended) A system[, organism or process] according to [any of claims 10-24] claim 10 wherein the plurality of extension modules corresponds to the extension modules of a PKS selected from erythromycin, narbomycin, pikromycin, lankamycin, kujimycin or megalomycin or a mutant or variant thereof able to direct synthesis of a macrolide.

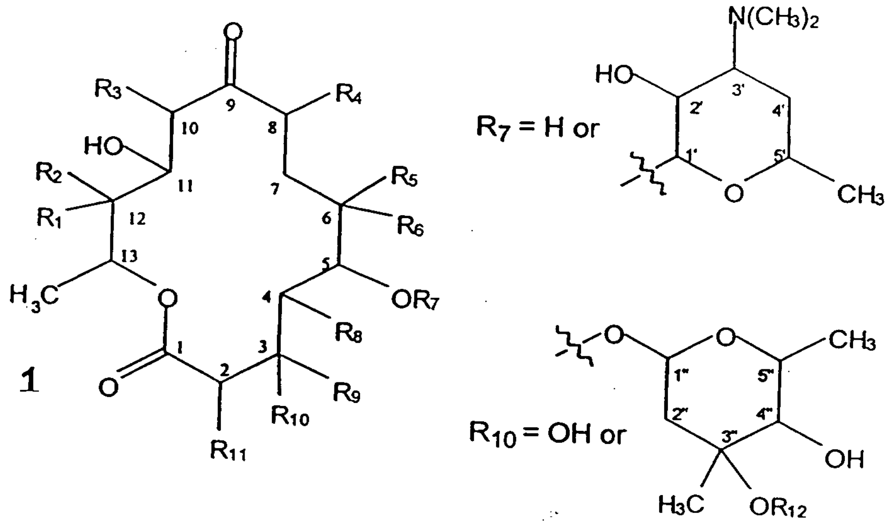
Add new claims 26-30, as follows:

A3

26. A PKS multienzyme which comprises a loading module and a plurality of extension modules, wherein said loading module is adapted to load a malonyl residue and then to effect a decarboxylation of the loaded residue to provide an acetate starter unit which is transferred to an adjacent one of said extension modules; and wherein at least one of the extension modules is not naturally associated with a loading module that effects decarboxylation.

27. A PKS multienzyme according to claim 26 which is adapted to synthesize a compound of the formula 1:

A3 cont.



1

or a pharmaceutically acceptable salt thereof, wherein R_1 is H or OH; R_2-R_4 are each independently H, CH_3, or CH_2CH_3; R_5 is H or OH; and R_6 is H, CH_3, or CH_2CH_3; R_7 is H or desosamine; R_8 is H, CH_3, or CH_2CH_3; R_9 is OH, mycarose (R_{12} is H), or cladinose (R_{12} is CH_3), R_{10} is H; or $R_9 = R_{10} = O$; and R_{11} is H, CH_3, or CH_2CH_3, with the proviso that when R_2-R_4 are CH_3, R_6 is CH_3, R_8 is CH_3, and R_{11} is CH_3, then R_1 and R_5 are not H and R_{12} is not H; or also when R_2-R_4 are CH_3, R_6 is CH_3, R_8 is CH_3, and R_{11} is CH_3, then R_1 and R_5 are not OH and R_{12} is not H.

A3 cont.

28. A process according to claim 7 which comprises culturing a transformant organism which comprises a system comprising DNA encoding and arranged to express a PKS multienzyme which comprises a loading module and a plurality of extension modules; wherein in the expressed multienzyme, said loading module is adapted to load a malonyl residue and then to effect a decarboxylation of the loaded residue to provide an acetate starter unit which is transferred to an adjacent one of said extension modules; and wherein at least one of the extension modules, is not naturally associated with a loading module that effects decarboxylation; and recovering a compound of formula 1.

29. An organism according to claim 22 wherein the plurality of extension modules corresponds to the extension modules of a PKS selected from erythromycin, narbomycin, pikromycin, lankamycin, kujimycin or megalomycin or a mutant or variant thereof able to direct synthesis of a macrolide.

30. A process according to claim 28 wherein the plurality of extension modules corresponds to the extension modules of a PKS selected from erythromycin, narbomycin, pikromycin, lankamycin, kujimycin or megalomycin or a mutant or variant thereof able to direct synthesis of a macrolide.

Please cancel claims 19, 23 and 24.